

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY TO CYTOKININ  
RECEPTOR

<130> P152622

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 3531

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(3531)

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Met Ser Ile Thr Cys Glu Leu Leu Asn Leu Thr Ser Lys Lys Ala Lys

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aag tcg tcg agc agt gac aag aaa tgg cta aag aag cct ctc ttc ttc 96

Lys Ser Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe

20 25 30

ctg att ttg tgt ggc tct ttg gta att gtt ttg gtt atg ttc tta cgg 144

Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg

35 40 45

tta ggt aga agt cag aag gag gag aca gat tct tgt aat gga gaa gag 192

Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu

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aaa gtg ttg tat aga cat caa aat gtc aca aga agt gag att cat gat 240

Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp

65 70 75 80

ttg gtc tct ttg ttc tct gat tca gat cag gta aca tcc ttt gaa tgt 288

Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys

85 90 95

cat aag gaa tca agc cct gga atg tgg aca aac tat ggt att aca tgt 336

His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys

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tcc ctg agt gtg cgt tct gat aaa caa gag act aga ggg ctt ccc tgg 384

Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp

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aat ctt ggc tta gga cat tct atc tca tca aca tct tgt atg tgt ggt 432

Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly

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aat ctt gaa ccg att tta cag caa cct gaa aac ctt gag gaa gaa aac 480

Asn Leu Glu Pro Ile Leu Gln Gln Pro Glu Asn Leu Glu Glu Glu Asn

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cat gaa gaa ggg ctg gag cag ggt ttg tca tcg tat tta aga aat gca 528

His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala

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tgg tgg tgt cta atc ctt ggt gtg tta gtg tgc cat aag att tat gta 576

Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val

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tct cat tct aaa gca cga ggt gag agg aaa gag aaa gta cat ctg caa 624

Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln

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gag gct tta gct cca aag aag cag caa caa cgt gct cag act tct tct 672

Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser

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aga ggg gct gga aga tgg agg aag aat atc ctt ctc ctt ggt att tta 720

Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu

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gga gga gtt tcc ttc tct gtt tgg tgg ttt tgg gac act aat gag gag 768

Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu

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atc ata atg aaa agg agg gag act ttg gca aac atg tgt gac gaa cga 816

Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg

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gca cgt gtt tta caa gat cag ttc aat gtt agc ttg aac cat gtt cat 864

Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His

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gcc ttg tct att ctt gta tct aca ttt cat cat ggt aaa atc cca tct 912

Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser

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gcc att gat cag aga aca ttt gaa gaa tat act gag aga aca aac ttt 960

Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe

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gag agg cca ctt act agt ggt gta gcg tat gct ttg aaa gtc cca cac 1008

Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His

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tca gaa aga gag aaa ttt gaa aag gag cat gga tgg gca ata aag aaa 1056

Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys

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atg gaa act gag gac cag aca gtt gta caa gat tgt gtt cct gaa aac 1104

Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn

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ttt gat ccc gca ccg att caa gac gaa tac gcg cca gtt ata ttt gct 1152

Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala

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caa gaa act gtt tcc cat att gta tcg gtc gac atg atg tct gga gaa 1200

Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu

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gaa gac cgt gaa aac atc tta cgg gca agg gca tca gga aaa gga gtg 1248

Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Ala Ser Gly Lys Gly Val

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tta aca tct cca ttt aag ctt ctt aag tca aat cat ctt ggt gtt gtg 1296

Leu Thr Ser Pro Phe Lys Leu Leu Lys Ser Asn His Leu Gly Val Val

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ttg acc ttt gct gtc tat gac acg agc cta ccg cct gat gct aca gaa			1344
Leu Thr Phe Ala Val Tyr Asp Thr Ser Leu Pro Pro Asp Ala Thr Glu			
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gaa cag cgt gtt gaa gca act att ggg tac ctt ggt gca tca tat gat			1392
Glu Gln Arg Val Glu Ala Thr Ile Gly Tyr Leu Gly Ala Ser Tyr Asp			
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atg cca tcg ctg gtg gag aaa ctt ctt cac caa ctt gcc agc aaa cag			1440
Met Pro Ser Leu Val Glu Lys Leu Leu His Gln Leu Ala Ser Lys Gln			
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aca att gct gtg gat gtt tac gac aca act aac act tca ggt cta ata			1488
Thr Ile Ala Val Asp Val Tyr Asp Thr Thr Asn Thr Ser Gly Leu Ile			
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aaa atg tat ggc tca gaa att ggg gat ata agt gag cag cat ata agt			1536
Lys Met Tyr Gly Ser Glu Ile Gly Asp Ile Ser Glu Gln His Ile Ser			
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agc ctt gat ttt ggt gat cca tca agg aac cat gag atg cat tgc agg 1584

Ser Leu Asp Phe Gly Asp Pro Ser Arg Asn His Glu Met His Cys Arg  
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ttt aag cat aaa ctt ccc att ccc tgg aca gcg ata aca ccg tgc atc 1632

Phe Lys His Lys Leu Pro Ile Pro Trp Thr Ala Ile Thr Pro Ser Ile  
530 535 540

tta gtt ctg gtt att act ttt ctt gtt ggt tat att tta tat gaa gcc 1680

Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala  
545 550 555 560

atc aac cga att gcg aca gtt gaa gag gat tgt cag aag atg agg gaa 1728

Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu  
565 570 575

ctc aaa gct cgt gct gag gcc gct gac att gca aag tca cag ttc cta 1776

Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu  
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gca act gtt tct cat gag ata cgg act ccg atg aat gga gtt tta gga 1824

Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly

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Met Leu Lys Met Leu Met Asp Thr Asp Leu Asp Ala Lys Gln Met Asp

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tat gcg caa act gct cat ggc agt ggg aag gat ctt aca tca cta ata 1920

Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile

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aat gag gtt ctt gat cag gca aag att gaa tcc gga agg ctc gag ctt 1968

Asn Glu Val Leu Asp Gln Ala Lys Ile Glu Ser Gly Arg Leu Glu Leu

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gaa aat gtg cct ttt gat atg cgt ttt att ctt gat aat gtt tca tct 2016

Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser

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ctc ctc tct ggc aag gca aat gaa aaa gga att gag ttg gcc gtt tat 2064

Leu Leu Ser Gly Lys Ala Asn Glu Lys Gly Ile Glu Leu Ala Val Tyr

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gtt tct agt caa gtt cct gat gtt gta gtc ggt gat ccg agt cgg ttc 2112

Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe

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cgg cag atc att aca aac ctg gtt gga aac tca atc aaa ttc aca cag 2160

Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln

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gaa agg gga cac ata ttt atc tca gtg cac ctt gca gat gag gta aag 2208

Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys

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gga tgc agc gag tcc ggt gag aca gtt agc ggg ttt cct gcg gta aat 2304

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Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met

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caa gcc gac agt tcc aca tcg cgg act tat ggt gga act ggc ata ggt 2496

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Leu Ser Ile Ser Lys Arg Leu Val Glu Leu Met Gln Gly Glu Met Gly

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ttt gtg agt gag ccc ggg ata ggc agt act ttt tca ttt act gga gtt 2592

Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val

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Phe Gly Lys Ala Glu Thr Asn Thr Ser Ile Thr Lys Leu Glu Arg Phe

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gat cta gct att cag gag ttt aca gga ttg aga gca tta gtt att gat 2688

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Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys

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tgt atc agc aaa tta gaa aat ttg gct atg att cta ata gac aaa gac 2832

Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp  
930 935 940

gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga 2880

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agc aaa gta acc ttt aca aga gtc cca aag att ttt ctt ttg gca act 2928

Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr  
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Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile  
980 985 990

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995 1000 1005

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cga aga aat ctt gga cac ttg cta aga gaa aaa cag att ctg gtt gtg 3120

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atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag 3264

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atg ttc tgt aaa ttt agt agt tgg cac gtc ccg ata tta gca atg aca 3408

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Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met

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gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg 3504

Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Val Leu Tyr Thr Ala

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25

30

Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg

35

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45

Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu

50

55

60

Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp

65

70

75

80

Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys

85

90

95

His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys

100

105

110

Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp

115

120

125



Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly  
 130 135 140  
 Asn Leu Glu Pro Ile Leu Gln Gln Pro Glu Asn Leu Glu Glu Glu Asn  
 145 150 155 160  
 His Glu Glu Gly Leu Glu Gln Gly Leu Ser Ser Tyr Leu Arg Asn Ala  
 165 170 175  
 Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val  
 180 185 190  
 Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln  
 195 200 205  
 Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser  
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 Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu  
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 Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu  
 245 250 255  
 Ile Ile Met Lys Arg Arg Glu Thr Leu Ala Asn Met Cys Asp Glu Arg  
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 Ala Arg Val Leu Gln Asp Gln Phe Asn Val Ser Leu Asn His Val His  
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 Ala Leu Ser Ile Leu Val Ser Thr Phe His His Gly Lys Ile Pro Ser  
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 Ala Ile Asp Gln Arg Thr Phe Glu Glu Tyr Thr Glu Arg Thr Asn Phe  
 305 310 315 320  
 Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala Leu Lys Val Pro His  
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Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys  
 340 345 350  
 Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn  
 355 360 365  
 Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala  
 370 375 380  
 Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu  
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 Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Ala Ser Gly Lys Gly Val  
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 Glu Gln Arg Val Glu Ala Thr Ile Gly Tyr Leu Gly Ala Ser Tyr Asp  
 450 455 460  
 Met Pro Ser Leu Val Glu Lys Leu Leu His Gln Leu Ala Ser Lys Gln  
 465 470 475 480  
 Thr Ile Ala Val Asp Val Tyr Asp Thr Thr Asn Thr Ser Gly Leu Ile  
 485 490 495  
 Lys Met Tyr Gly Ser Glu Ile Gly Asp Ile Ser Glu Gln His Ile Ser  
 500 505 510  
 Ser Leu Asp Phe Gly Asp Pro Ser Arg Asn His Glu Met His Cys Arg  
 515 520 525  
 Phe Lys His Lys Leu Pro Ile Pro Trp Thr Ala Ile Thr Pro Ser Ile  
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Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala  
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 Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu  
                          565                      570                      575  
 Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu  
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 Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly  
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 Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile  
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 Asn Glu Val Leu Asp Gln Ala Lys Ile Glu Ser Gly Arg Leu Glu Leu  
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 Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser  
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 Leu Leu Ser Gly Lys Ala Asn Glu Lys Gly Ile Glu Leu Ala Val Tyr  
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 Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe  
                          690                      695                      700  
 Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln  
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 Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys  
                          725                      730                      735  
 Glu Pro Leu Thr Ile Glu Asp Ala Val Leu Lys Gln Arg Leu Ala Leu  
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Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr			
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Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile			
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Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys			
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Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln			
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Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val			
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Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys			
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Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala			
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Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln			
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Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu			
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Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu			
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Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr			
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Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met			
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Val Ala Arg Phe Phe Glu Pro Cys

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Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly

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30

atc gag gac aag tct ggt ctt tta gtt ggc tct gtc ggt gat ctt gag 144

Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu

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aag act aag atg act acg ttg aag aag aag aac aag atg tgg ttc tgg 192

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp

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aat aag atc tct agc agc gga ctc aag atc ccg agt ttc tct tat cag 240

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln

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75

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ttt ctt ggc tct gtt aaa ttc aac aag gcg tgg tgg agg aag ctt gtg 288

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90

95

gtg gtt tgg gtt gtc ttc tgg gtc ttg gtc tct att tgg acg ttt tgg 336

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp

100

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110

tac ttt agc tcg caa gct atg gag aag agg aaa gag acg cta gct agt 384

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser

115

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125

atg tgt gat gag aga gct cgt atg ctg cag gat cag ttc aac gtt agc 432

Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

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atg aat cat gtt caa gcc atg tct atc ttg atc tca acc ttc cac cat 480

Met Asn His Val Gln Ala Met Ser Ile Leu Ile Ser Thr Phe His His

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160

ggc aag att cct tct gct atc gat cag aga aca ttc tca gag tac act 528

Gly Lys Ile Pro Ser Ala Ile Asp Gln Arg Thr Phe Ser Glu Tyr Thr

165

170

175

gat aga act tcc ttt gag agg cct ctt act agc ggg gta gct tat gct 576

Asp Arg Thr Ser Phe Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala

180

185

190

atg agg gtg ctc cat tca gag agg gaa gag ttc gag agg caa caa ggt 624

Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly



195

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tgg act att agg aag atg tat tct ctt gaa caa aac cca gtt cac aag 672

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215

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265

270

agg agt tca ggt aaa ggg gtt ttg aca gct cct ttc cca ttg ata aag 864

Arg Ser Ser Gly Lys Gly Val Leu Thr Ala Pro Phe Pro Leu Ile Lys

275

280

285

aca aat aga ctt ggg gtg atc ctg aca ttt gca gtg tac aag aga gat 912

Thr Asn Arg Leu Gly Val Ile Leu Thr Phe Ala Val Tyr Lys Arg Asp  
290 295 300

ctc ccc tcc aat gca acg cca aaa gag aga att gag gct act aac ggg 960

Leu Pro Ser Asn Ala Thr Pro Lys Glu Arg Ile Glu Ala Thr Asn Gly  
305 310 315 320

tat ctc ggg gga gtg ttt gac att gag tcc ctg gta gaa aac tlg ctt 1008

Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu  
325 330 335

caa cag ctg gct agc aag caa acg att ctt gtc aat gtg tac gat atc 1056

Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile  
340 345 350

acc aat cac tct caa ccg att agc atg tat ggt aca aat gtg tgc gct 1104

Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala  
355 360 365

gat ggg ttg gaa cgt gtt agt cca cta atc ttt ggc gat cca ttg aga 1152

Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg  
370 375 380

aag cat gag atg cgt tgc aga ttt aag cag aaa cca cca tgg cca gtg 1200

Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val  
385 390 395 400

cta tca atg gtg aca tca ttc ggt atc ctt gtg att gcg tta ctt gtt 1248

Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val  
405 410 415

gca cat ata atc cac gca acc gtt agt cga ata cac aaa gtt gaa gaa 1296

Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu  
420 425 430

gat tgt gat aaa atg aag cag ctc aag aaa aag gct gaa gca gca gat 1344

Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp  
435 440 445

gtt gca aag tca cag ttc ctt gcc act gtt tca cat gaa atc aga act 1392

Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr

450

455

460

cca atg aat ggt gtt cta gga atg ttg cat atg ctt atg gac aca gag 1440

Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu

465

470

475

480

tta gat gtt acg caa cag gat tat gtt agg acc gca cag gca agt gga 1488

Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly

485

490

495

aaa gct tta gtc tcg cta ata aat gag gtt ttg gac caa gca aag att 1536

Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile

500

505

510

gaa tct gga aag ctt gaa ctt gag gag gtg cgg ttt gat ttg aga gga 1584

Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly

515

520

525

ata tta gat gat gtc ctg tca ctc ttc tct agc aag tcc caa caa aag 1632

Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys

530

535

540

ggg gtg gag ttg gca gta tac ata tct gat cgt gtt cca gat atg tta 1680

Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu

545

550

555

560

att ggt gat cct ggg agg ttt cga caa ata ctc aca aat ctt atg ggt 1728

Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly

565

570

575

aat tcc att aag ttc act gag aaa gga cac atc ttt gta act gtt cat 1776

Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His

580

585

590

ttg gtg gat gag cta ttt gaa tct atc gat gga gag aca gca tca tct 1824

Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser

595

600

605

ccg gaa agt aca ctg agt ggg ctt cca gtt gca gac cgg cag agg agc 1872

Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser

610

615

620

tgg gaa aac ttt aaa gct ttc agc tcc aac ggg cat cgg agc ttt gaa 1920

Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu

625

630

635

640

cca tct ccc cct gat ata aac cta atc gtc tca gtt gag gat act ggc 1968

Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly

645

650

655

gta ggg atc cct gta gaa gcg cag tcc cgt att ttt acg cct ttc atg 2016

Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met

660

665

670

caa gtc gga cca tcc ata tcc agg acg cat gga ggc aca gga att gga 2064

Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly

675

680

685

ctt agc ata agc aaa tgt cta gtt gga ctg atg aag gga gaa att gga 2112

Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly

690

695

700

ttc tcg agt act ccc aag gtt ggg tcc aca ttc aca ttt act gct gta 2160

Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val  
705 710 715 720

ttt tcc aat ggg atg caa cca gct gaa aga aag aat gac aac aac cag 2208

Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln  
725 730 735

ccc ata ttc tcg gaa ttc cgg ggc atg aaa gct gtg gtt gtg gac cat 2256

Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His  
740 745 750

agg cct gca agg gca aaa gtc tcg tgg tac cat ttt cag cgt ctt gga 2304

Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly  
755 760 765

att cga gtc gaa gta gtt cca cgt gtt gaa cag gct cta cat tat ctg 2352

Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu  
770 775 780

aag att ggt act acc act gtg aat atg ata ctc ata gag caa gaa ata 2400

Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile

785

790

795

800

tgg aat agg gaa gca gat gat ttc att aaa aag cta cag aaa gac cct 2448

Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro

805

810

815

ctt ttc ctt tct cct aag ttg att ttg tta gca aac tca gta gaa tcg 2496

Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser

820

825

830

tca ata tca gag gct tta tgc acc ggt ata gat cct cca ata gtg ata 2544

Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile

835

840

845

gtg aaa cca ttg agg gcg agt atg cta gca gca act ttg cag agg gga 2592

Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly

850

855

860

ttg ggt att gga atc aga gaa cca cct caa cac aag gga cct cct gct 2640



Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala

865

870

875

880

ttg att ctc agg aat ctt ctc ctt ggt aga aaa att tta atc gtg gat 2688

Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp

885

890

895

gat aac aac gta aac ctc aga gtg gca gcg gga gct ctg aaa aag tac 2736

Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr

900

905

910

gga gct gat gtg gtc tgc gct gag agt ggg ata aag gca atc tca ttg 2784

Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu

915

920

925

ctt aag cca cct cac gag ttt gat gct tgc ttc atg gac att cag atg 2832

Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met

930

935

940

cca gaa atg gat gga ttt gaa gct aca agg aga ata cga gat atg gaa 2880

Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu

945 950 955 960

gag gag atg aac aag aga ata aag aat ggg gag gct ttg ata gta gag 2928

Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu

965 970 975

aac ggt aac aaa aca agc tgg cat ctt ccg gta tta gca atg acg gca 2976

Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala

980 985 990

gat gtg atc caa gca acg cat gag gaa tgt ctg aag tgt gga atg gat 3024

Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp

995 1000 1005

ggg tat gta tca aaa cca ttt gaa gca gag cag ctg tac agg gaa gtt 3072

Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val

1010 1015 1020

tct cgc ttt ttc aat tcg cct tca gat aca gaa tca taa 3111

Ser Arg Phe Phe Asn Ser Pro Ser Asp Thr Glu Ser

1025

1030

1035

&lt;210&gt; 4

&lt;211&gt; 1036

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 4

Met Ser Leu Phe His Val Leu Gly Phe Gly Val Lys Ile Gly His Leu

1

5

10

15

Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly

20

25

30

Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu

35

40

45

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp

50

55

60

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln

65

70

75

80

Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val

85

90

95

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp

100

105

110

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser

115

120

125

Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

130	135	140			
Met Asn His Val Gln Ala	Met Ser Ile Leu Ile	Ser Thr Phe His His			
145	150	155	160		
Gly Lys Ile Pro Ser Ala	Ile Asp Gln Arg Thr Phe	Ser Glu Tyr Thr			
	165	170	175		
Asp Arg Thr Ser Phe Glu	Arg Pro Leu Thr Ser Gly	Val Ala Tyr Ala			
	180	185	190		
Met Arg Val Leu His Ser	Glu Arg Glu Glu Phe Glu	Arg Gln Gln Gly			
	195	200	205		
Trp Thr Ile Arg Lys Met	Tyr Ser Leu Glu Gln Asn	Pro Val His Lys			
	210	215	220		
Asp Asp Tyr Asp Leu Glu	Ala Leu Glu Pro Ser Pro	Val Gln Glu Glu			
225	230	235	240		
Tyr Ala Pro Val Ile Phe	Ala Gln Asp Thr Val Ser	His Val Val Ser			
	245	250	255		
Leu Asp Met Leu Ser Gly	Lys Glu Asp Arg Glu Asn	Val Leu Arg Ala			
	260	265	270		
Arg Ser Ser Gly Lys Gly	Val Leu Thr Ala Pro Phe	Pro Leu Ile Lys			
	275	280	285		
Thr Asn Arg Leu Gly Val	Ile Leu Thr Phe Ala Val	Tyr Lys Arg Asp			
	290	295	300		
Leu Pro Ser Asn Ala Thr	Pro Lys Glu Arg Ile Glu	Ala Thr Asn Gly			
305	310	315	320		
Tyr Leu Gly Gly Val Phe	Asp Ile Glu Ser Leu Val	Glu Asn Leu Leu			
	325	330	335		
Gln Gln Leu Ala Ser Lys	Gln Thr Ile Leu Val Asn	Val Tyr Asp Ile			

340	345	350
Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala		
355	360	365
Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg		
370	375	380
Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val		
385	390	395
Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val		
405	410	415
Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu		
420	425	430
Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp		
435	440	445
Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr		
450	455	460
Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu		
465	470	475
Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly		
485	490	495
Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile		
500	505	510
Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly		
515	520	525
Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys		
530	535	540
Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu		

545                      550                      555                      560  
 Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly  
                     565                      570                      575  
 Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His  
                     580                      585                      590  
 Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser  
                     595                      600                      605  
 Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser  
                     610                      615                      620  
 Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu  
 625                      630                      635                      640  
 Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly  
                     645                      650                      655  
 Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met  
                     660                      665                      670  
 Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly  
                     675                      680                      685  
 Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly  
                     690                      695                      700  
 Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val  
 705                      710                      715                      720  
 Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln  
                     725                      730                      735  
 Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His  
                     740                      745                      750  
 Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly

755	760	765
Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu		
770	775	780
Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile		
785	790	795
Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro		
805	810	815
Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser		
820	825	830
Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile		
835	840	845
Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly		
850	855	860
Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala		
865	870	875
Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp		
885	890	895
Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr		
900	905	910
Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu		
915	920	925
Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met		
930	935	940
Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu		
945	950	955
Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu		

	965	970	975
Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala			
980	985	990	
Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp			
995	1000	1005	
Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val			
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Ser Arg Phe Phe Asn Ser Pro Ser Asp Thr Glu Ser			
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Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg

1

5

10

15



aga att gaa att tct gat tcc gag tca cta gaa aac ttg aaa agc agc 96

Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser

20

25

30

gat ttt tat caa ctg ggt ggt ggt ggt gct ctg aat tcg tca gaa aag 144

Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys

35

40

45

ccg aga aag atc gat ttt tgg cgt tcg ggg ttg atg ggt ttt gcg aag 192

Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys

50

55

60

atg cag cag cag caa cag ctt cag cat tca gtg gcg gtg aag atg aac 240

Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn

65

70

75

80

aat aat aat aat aac gat cta atg ggt aat aaa aaa ggg tca act ttc 288

Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe

85

90

95

ata caa gaa cat cga gca ttg tta cca aaa gct ttg att ctg tgg atc 336

Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile

100

105

110

atc att gtt ggg ttt ata agc agt ggg att tat cag tgg atg gat gat 384

Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp

115

120

125

gct aat aag att aga agg gaa gag gtt ttg gtc agc atg tgt gat caa 432

Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln

130

135

140

aga gct aga atg ttg cag gat caa ttt agt gtt agt gtt aat cat gtt 480

Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val

145

150

155

160

cat gct ttg gct att ctc gtc tcc act ttt cat tac cac aag aac cct 528

His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro

165

170

175

tct gca att gat cag gag aca ttt gcg gag tac acg gca aga aca gca 576

Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala

180

185

190

ttt gag aga ccg ttg cta agt gga gtg gct tat gct gaa aaa gtt gtg 624

Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val

195

200

205

aat ttt gag agg gag atg ttt gag cgg cag cac aat tgg gtt ata aag 672

Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys

210

215

220

aca atg gat aga gga gag cct tca ccg gtt agg gat gag tat gct cct 720

Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro

225

230

235

240

gtt ata ttc tct caa gat agt gtc tct tac ctt gag tca ctc gat atg 768

Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met

245

250

255

atg tca ggc gag gag gat cgt gag aat att ttg cga gct aga gaa acc 816

Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr

260

265

270

gga aaa gct gtc ttg act agc cct ttt agg ttg ttg gaa act cac cat 864

Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His

275

280

285

ctc gga gtt gtg ttg aca ttc cct gtc tac aag tct tct ctt cct gaa 912

Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu

290

295

300

aat ccg act gtc gaa gag cgt att gca gcc act gca ggg tac ctt ggt 960

Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly

305

310

315

320

ggt gcg ttt gat gtg gag tct cta gtc gag aat tta ctt ggt cag ctt 1008

Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu

325

330

335

gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca 1056

Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala

340

345

350

tca gat cca ctt gtc atg tat ggt aat caa gat gaa gaa gcc gac aga 1104

Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg

355

360

365

tct ctc tct cat gag agc aag ctc gat ttt gga gac ccc ttc agg aaa 1152

Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys

370

375

380

cat aag atg ata tgc agg tac cac caa aag gca cca ata cca ttg aat 1200

His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn

385

390

395

400

gtg ctc aca act gtg cca ttg ttc ttt gcg att ggt ttc ttg gtg ggt 1248

Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly

405

410

415

tat ata ctg tat ggt gca gct atg cac ata gta aaa gtc gaa gat gat 1296

Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp

420

425

430

ttc cat gaa atg caa gag ctt aaa gtg cga gca gaa gct gct gat gtc 1344

Phe His Glu Met Gln Glu Leu Lys Val Arg Ala Glu Ala Ala Asp Val

435

440

445

gct aaa tcg cag ttt ctt gct acc gtg tct cac gag atc agg aca cca 1392

Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr Pro

450

455

460

atg aat ggc att ctc gga atg ctt gct atg ctc cta gat aca gaa cta 1440

Met Asn Gly Ile Leu Gly Met Leu Ala Met Leu Leu Asp Thr Glu Leu

465

470

475

480

agc tcg aca cag aga gat tac gct caa acc gct caa gta tgt ggt aaa 1488

Ser Ser Thr Gln Arg Asp Tyr Ala Gln Thr Ala Gln Val Cys Gly Lys

485

490

495

gct ttg att gca ttg ata aat gag gtt ctt gat cgc gcc aag att gaa 1536

Ala Leu Ile Ala Leu Ile Asn Glu Val Leu Asp Arg Ala Lys Ile Glu

500

505

510

gct gga aag ctg gag ttg gaa tca gta cca ttt gat atc cgt tca ata 1584

Ala Gly Lys Leu Glu Leu Glu Ser Val Pro Phe Asp Ile Arg Ser Ile

515

520

525

ttg gat gat gtc ctt tct cta ttc tct gag gag tca agg aac aaa ggc 1632

Leu Asp Asp Val Leu Ser Leu Phe Ser Glu Glu Ser Arg Asn Lys Gly

530

535

540

att gag ctc gcg gtt ttc gtt tca gac aaa gta cca gag ata gtc aaa 1680

Ile Glu Leu Ala Val Phe Val Ser Asp Lys Val Pro Glu Ile Val Lys

545

550

555

560

gga gat tca ggg aga ttt aga cag ata atc ata aac ctt gtt gga aat 1728

Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn

565

570

575

tcg gtt aaa ttc aca gag aaa gga cat atc ttt gtt aaa gtc cat ctt 1776

Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu

580

585

590

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt 1824

Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly

595

600

605

gga gtg tct gaa gaa atg atc gtt gtt tcc aaa cag tca agt tac aac 1872

Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn

610

615

620

aca ttg agc ggt tac gaa gct gct gat ggt cgg aat agc tgg gat tca 1920

Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser

625

630

635

640

ttc aag cat ttg gtc tct gag gag cag tca tta tcg gag ttt gat att 1968

Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile

645

650

655

tct agc aat gtt agg ctt atg gtt tca atc gaa gac acg ggt att gga 2016

Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly

660

665

670

atc cct tta gtt gca caa ggc cgt gtg ttt atg ccg ttt atg caa gca 2064



Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala

675

680

685

gat agc tcg act tca aga aac tat gga ggt act ggt att ggt ttg agt 2112

Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser

690

695

700

ata agc aag tgt ctt gtt gaa ctt atg cgt ggt cag ata aat ttc ata 2160

Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile

705

710

715

720

agc cgg cct cat att gga agc acg ttc tgg ttc acg gct gtt tta gag 2208

Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu

725

730

735

aaa tgc gat aaa tgc agt gcg att aac cat atg aag aaa cct aat gtg 2256

Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val

740

745

750

gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat 2304

Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp

755

760

765

gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc 2352

Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu

770

775

780

gga atc aat gtt gat gtc gtg aca agt ctc aaa acc gct gtt gtt gca 2400

Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala

785

790

795

800

gct gct gcg ttt gaa aga aac ggt tct cct ctc cca aca aaa ccg caa 2448

Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln

805

810

815

ctt gat atg atc tta gta gag aaa gat tca tgg att tca act gaa gat 2496

Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp

820

825

830

aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt 2544

Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val

835

840

845

cat cac aag tct ccg aaa cta gct cta ttc gca aca aac atc aca aat 2592

His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn

850

855

860

tcg gag ttc gac aga gct aaa tcc gca gga ttt gca gat acg gta ata 2640

Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile

865

870

875

880

atg aaa ccg tta aga gca agc atg att ggg gcg tgt ctg caa caa gtt 2688

Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val

885

890

895

ctc gag ctg aga aaa aca aga caa caa cat cca gaa gga tca tca ccc 2736

Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro

900

905

910

gca act ctc aag agc ttg ctt aca ggg aag aag att ctt gtg gtt gat 2784

Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp

915

920

925

gat aat ata gtt aac agg aga gta gct gca gga gct ctc aag aaa ttt 2832

Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe

930

935

940

gga gca gaa gtg gtt tgt gca gag agt ggt caa gtt gct ttg ggt ttg 2880

Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu

945

950

955

960

ctt cag att cca cac act ttc gat gct tgc ttc atg gat att caa atg 2928

Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met

965

970

975

cca cag atg gac gga ttt gaa gca act cgt cag ata aga atg atg gag 2976

Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu

980

985

990

aag gaa gct aaa gag aag acg aat ctc gaa tgg cat tta ccg att cta 3024

Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu

995

1000

1005

gcg atg act gcg gat gtg ata cac gcg acc tac gag gaa tgt ctg aaa 3072

Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys

1010

1015

1020

agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc 3120

Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu

1025

1030

1035

1040

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168

Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser

1045

1050

1055

tcg taa

3174

Ser

<210> 6

<211> 1057

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg

1                      5                      10                      15  
 Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser  
                     20                      25                      30  
 Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys  
                     35                      40                      45  
 Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys  
                     50                      55                      60  
 Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn  
                     65                      70                      75                      80  
 Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe  
                     85                      90                      95  
 Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile  
                     100                      105                      110  
 Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp  
                     115                      120                      125  
 Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln  
                     130                      135                      140  
 Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val  
                     145                      150                      155                      160  
 His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro  
                     165                      170                      175  
 Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala  
                     180                      185                      190  
 Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val  
                     195                      200                      205  
 Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys

210	215	220	
Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro			
225	230	235	240
Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met			
	245	250	255
Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr			
	260	265	270
Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His			
	275	280	285
Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu			
	290	295	300
Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly			
305	310	315	320
Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu			
	325	330	335
Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala			
	340	345	350
Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg			
	355	360	365
Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys			
	370	375	380
His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn			
385	390	395	400
Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly			
	405	410	415
Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp			

			420					425						430		
Phe	His	Glu	Met	Gln	Glu	Leu	Lys	Val	Arg	Ala	Glu	Ala	Ala	Asp	Val	
		435						440						445		
Ala	Lys	Ser	Gln	Phe	Leu	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	
		450						455						460		
Met	Asn	Gly	Ile	Leu	Gly	Met	Leu	Ala	Met	Leu	Leu	Asp	Thr	Glu	Leu	
465								470						475		480
Ser	Ser	Thr	Gln	Arg	Asp	Tyr	Ala	Gln	Thr	Ala	Gln	Val	Cys	Gly	Lys	
					485					490						495
Ala	Leu	Ile	Ala	Leu	Ile	Asn	Glu	Val	Leu	Asp	Arg	Ala	Lys	Ile	Glu	
					500					505						510
Ala	Gly	Lys	Leu	Glu	Leu	Glu	Ser	Val	Pro	Phe	Asp	Ile	Arg	Ser	Ile	
					515					520						525
Leu	Asp	Asp	Val	Leu	Ser	Leu	Phe	Ser	Glu	Glu	Ser	Arg	Asn	Lys	Gly	
		530							535					540		
Ile	Glu	Leu	Ala	Val	Phe	Val	Ser	Asp	Lys	Val	Pro	Glu	Ile	Val	Lys	
545									550					555		560
Gly	Asp	Ser	Gly	Arg	Phe	Arg	Gln	Ile	Ile	Ile	Asn	Leu	Val	Gly	Asn	
					565						570					575
Ser	Val	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Lys	Val	His	Leu	
					580						585					590
Ala	Glu	Gln	Ser	Lys	Asp	Glu	Ser	Glu	Pro	Lys	Asn	Ala	Leu	Asn	Gly	
					595						600					605
Gly	Val	Ser	Glu	Glu	Met	Ile	Val	Val	Ser	Lys	Gln	Ser	Ser	Tyr	Asn	
					610									615		620
Thr	Leu	Ser	Gly	Tyr	Glu	Ala	Ala	Asp	Gly	Arg	Asn	Ser	Trp	Asp	Ser	



625	630	635	640
Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile			
645	650	655	
Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly			
660	665	670	
Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala			
675	680	685	
Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser			
690	695	700	
Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile			
705	710	715	720
Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu			
725	730	735	
Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val			
740	745	750	
Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp			
755	760	765	
Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu			
770	775	780	
Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala			
785	790	795	800
Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln			
805	810	815	
Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp			
820	825	830	
Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val			

835	840	845
His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn		
850	855	860
Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile		
865	870	875
Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val		
885	890	895
Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro		
900	905	910
Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp		
915	920	925
Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe		
930	935	940
Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu		
945	950	955
Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met		
965	970	975
Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu		
980	985	990
Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu		
995	1000	1005
Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys		
1010	1015	1020
Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu		
1025	1030	1035
Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser		

1045

1050

1055

Ser

&lt;210&gt; 7

&lt;211&gt; 125

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 7

Glu Thr Ser Val Lys Ile Leu Val Val Glu Asp Asn His Val Asn Gln

1

5

10

15

Glu Val Ile Lys Arg Met Leu Asn Leu Glu Gly Ile Glu Asn Ile Glu

20

25

30

Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr

35

40

45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro

50

55

60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly

65

70

75

80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn

85

90

95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro

100

105

110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe

115

120

125

<210> 8

<211> 118

<212> PRT

<213> Escherichia coli

<400> 1

Asn Asp Asp Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg

1

5

10

15

Arg Leu Leu Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr

20

25

30

Ala Asn Asp Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile

35

40

45

Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg

50

55

60

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly

65

70

75

80

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser

85

90

95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys

100

105

110

Gln Ser Leu Thr Leu Tyr

115

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 9

tccccgcgga aaatgttctt acggttaggt ag

32

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 10

tcggtcgact tatgattctg tatctgaagg cga

33

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 11

tcagatatga actgggcact caac

24

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 12

ctcaatgcctt ttgttccttg actc

24

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for PCR

<400> 13

accatgaact gggcactcaa caatcatcaa g

31

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 14

ggattacgac gaaggtgaga taggattagg

30

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 15

gatcccagct agctagggcc ctaccgcggg ga

32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 16

tccccgcgga aaatgttcctt acggttaggt ag

32

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
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<400> 17

tcggtcgact tatgattctg tatcigaagg cga

33

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
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<400> 18

ctagtcctccg cggtagggcc ctagctagct gg

32

<210> 19

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 19

tccccgcgga aaatgtctat aacttgtag c

31

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 20

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33

<210> 21

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 21

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33

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed  
oligonucleotide primer for PCR

<400> 22

ctagctagct taacaagggtt caaagaattt gc

32